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Om protein - protein search, using sw model

Run on: December 26, 2001, 10:34:59 ; Search time 98.13 Seconds
 (without alignments)
 1324.197 Million cell updates/sec

Title: US-09-497-967-7
 Perfect score: 2540

Sequence: 1 MNNILVLLISLFINQIKS.....QCDFAFNLSISLLISYLL 468

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 4 summaries

Database : Pending_Patents_AA_Main:
 1: /cgns_6/picodata/2/paa/US075_COMB.pep:/*
 2: /cgns_6/picodata/2/paa/US06_COMB.pep:/*
 3: /cgns_6/picodata/2/paa/US07_COMB.pep:/*
 4: /cgns_6/picodata/2/paa/US080_COMB.pep:/*
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 24: /cgns_6/picodata/2/paa/US60_COMB.pep:/*

RESULT 1
 US-09-498-612-6

; Sequence 6, Application US/09498612
 ; GENERAL INFORMATION:
 ; APPLICANT: DICKERSON JR., Harry W.
 ; CLARK, Theodore G.
 ; APPLICANT: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC
 ; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN PROTOZOA
 ; FILE REFERENCE: 235_00100101
 ; CURRENT APPLICATION NUMBER: US/09/498-612
 ; PRIORITY FILING DATE: 2000-02-04
 ; PRIORITY NUMBER: 60/122,372
 ; PRIORITY NUMBER: 1999-03-02
 ; PRIORITY NUMBER: 60/124,905
 ; PRIORITY NUMBER: 1999-03-17
 ; PRIORITY NUMBER: 60/131,121
 ; PRIORITY NUMBER: 1999-04-27
 ; PRIORITY NUMBER: PCF/US00/02966
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 468
 ; TYPE: PRT
 ; ORGANISM: Ichthyophthirius multifiliis
 ; US-09-498-612-6

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2540	100.0	468	18	US-09-498-612-6	Sequence 6, Appli
2	921	36.3	442	18	US-09-498-612-6	Sequence 5, Appli
3	843.5	33.2	414	3	US-07-763-352A-15	Sequence 15, Appli
4	749	29.5	375	3	US-07-763-352A-15	Sequence 3, Appli
5	251	9.9	3131	19	PCT-US01-69696-02	Sequence 2, Appli
6	251	9.9	3131	19	US-09-515-365-2	Sequence 2, Appli
7	251	9.9	3131	19	US-09-515-365B-2	Sequence 2, Appli
8	245.5	9.7	3880	4	US-08-028-021-1	Sequence 1, Appli
9	242.5	9.5	544	21	US-09-791-932-40	Sequence 40, Appli

Query	Match	100 0%	Score 2540; DB 18;	Length 468;	
Best Local Similarity	100 0%	Pred. No. 3..le-213;			
Matches 468;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
1 MKNNILVILISLFTNQIKSANCPVGETAGQVDDLTGATTAQCNVCCNKNFYNNAAFY 60					
1 MKNNILVILISLFTNQIKSANCPVGETAGQVDDLTGATTAQCNVCCNKNFYNNAAFY 60					
0 PGASTCTPCPKDKDQAQPNPATANLVTCNCVCPGATAIAGGTDAIAITTECVNCRI 120					
61 PGASTCTPCPKDKDQAQPNPATANLVTCNCVCPGATAIAGGTDAIAITTECVNCRI 120					
0 NFYENAPNENAGASTCTACPVNRVGGALTAGNAATTIAQCNVACPTGTAIADDGVTYV 180					
121 NFYENAPNENAGASTCTACPVNRVGGALTAGNAATTIAQCNVACPTGTAIADDGVTYV 180					
0 RSFTECYKCRNFYNNGNGTIPFNGKSQSCPCKPAIKPANAQATLGNDAITAQCNVA 240					
181 RSFTECYKCRNFYNNGNGTIPFNGKSQSCPCKPAIKPANAQATLGNDAITAQCNVA 240					
0 CPDGTTISAGYNNWVACNTECTNCAPNFYNNNAPNPGNSTCLCPANKDYGAEATAGG 300					
241 CPDGTTISAGYNNWVACNTECTNCAPNFYNNNAPNPGNSTCLCPANKDYGAEATAGG 300					
0 AATLAKCNCNIACPDGTTISAGATNYVLTQETCLCAANNEFDGNNFEQASRSRKACPANK 360					
301 AATLAKCNCNIACPDGTTISAGATNYVLTQETCLCAANNEFDGNNFEQASRSRKACPANK 360					
0 YOGAVATGATTLIACALECPAGTVLTDGTTSTYKQAASECVCKAANYYTTKOTDWVA 420					
361 YOGAVATGATTLIACALECPAGTVLTDGTTSTYKQAASECVCKAANYYTTKOTDWVA 420					
b					
QY 1 MKNNILVILISLFTNQIKSANCPVGETAGQVDDLTGATTAQCNVACPTGTAIADDGVTYV 56					
Db 1 MKNNILVILISLFTNQIKSANCPVGETAGQVDDLTGATTAQCNVACPTGTAIADDGVTYV 56					
QY 57 AAFTPGASTCTPOPQQKDQAQPNPATANLVTCNCVCPGATAIAGGTDAIAITTECV 116					
Db 57 AA-----					
QY 117 NCRLNFYENAPNENAGASTCTACPVNRVGGALTAGNAATTIAQCNVACPTGTAIADDGVT 176					
Db 72 -----					
QY 117 TDYVRSFTECYKCRNFYNNGNGTIPFNGKSQSCPCKPAIKPANAQATLGNDAITAQCNVA 221					
Db 118 DVFRSAAUCVKCPKPNFTYNGGSFQGEAPGVQYFAAGAAAAGVAAVTSQSCVCPQLNR-N 175					
QY 222 VAQATLGNDAITAQCNVACPTGTAIADDGVTYV 272					
Db 176 DSPTAGADANLAUQCNSQSCPCKPAIKPANAQATLGNDAITAQCNVA 233					
QY 273 APN----					
Db 234 APGQVFAAGAAAAGVAAVTSQSCVCPQTNKQ-DSPATGQANIAQOCTQCPGTALQD 292					
QY 321 GAT-NVYILOTECNCNANFYFGDNNEQAGSSRCKACPAKVKQGAVATAGGTATLIACQA 379					
Db 293 GVTIYFSNSSTOCSCQIANFYENG-NFEAGKSQCLCPVSKTPAH-A-PGNTATQATQCL 350					
QY 380 LECPAGTVLTDGTTSTYKQAASECVCKAANYYTTKOTDWVAGTCTCSNKKTSGAFAN 439					
Db 351 TTCPACTVLDGTTNEVASATETKCSAGFFPAKTTGTAGTTCTCTKTTGATGATAK 410					
QY 440 LPESAKKNIOC--DFANFLSILLISLISLYLL 468					
Db 411 VYAAATQKVOCASSTFAKELSIISLIFISYLL 442					

RESULT 3
US-07-763-352A-15

Sequence 5, Application US/09498612

GENERAL INFORMATION:

APPLICANT: GAERTIG, Jacek

APPLICANT: DICKERSON, Harry W.

APPLICANT: CLARK, Theodore G.

APPLICANT: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC

TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN PROTOZOA

FILE REFERENCE: 235_00100101

CURRENT APPLICATION NUMBER: US/09498,612

CURRENT FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/118,634

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: 60/122,372

PRIOR FILING DATE: 1999-03-02

PRIOR APPLICATION NUMBER: 60/124,905

PRIOR FILING DATE: 1999-03-17

PRIOR APPLICATION NUMBER: 60/131,121

PRIOR FILING DATE: 1999-04-27

PRIOR APPLICATION NUMBER: PCT/US00/02966

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 442

TYPE: PRT

ORGANISM: Ichthyophthirius multifiliis

Query Match 36.3%; Score 921; DB 18; Length 442;

Best Local Similarity 41.8%; Pred. No. 1.3e-71;

Matches 214; Conservative 45; Mismatches 139; Indels 114; Gaps 19;

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 414 amino acids

RESULT 2
S-09-498-612-5

Sequence 5, Application US/09498612

GENERAL INFORMATION:

APPLICANT: CLARK, Theodore G.

APPLICANT: DICKERSON, Harry W.

APPLICANT: CLARK, Theodore G.

APPLICANT: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC

TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN PROTOZOA

FILE REFERENCE: 235_00100101

CURRENT APPLICATION NUMBER: US/09498,612

CURRENT FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/118,634

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: 60/122,372

PRIOR FILING DATE: 1999-03-02

PRIOR APPLICATION NUMBER: 60/124,905

PRIOR FILING DATE: 1999-03-17

PRIOR APPLICATION NUMBER: 60/131,121

PRIOR FILING DATE: 1999-04-27

PRIOR APPLICATION NUMBER: PCT/US00/02966

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.0

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 442

TYPE: PRT

ORGANISM: Ichthyophthirius multifiliis

Query Match 36.3%; Score 921; DB 18; Length 442;

Best Local Similarity 41.8%; Pred. No. 1.3e-71;

Matches 214; Conservative 45; Mismatches 139; Indels 114; Gaps 19;

TELEX: 823189

TELEFAX: 303/499-8089

TELEPHONE: 303/499-8080

RESULT 3
US-07-763-352A-15

Sequence 5, Application US/07763352A

GENERAL INFORMATION:

APPLICANT: Clark, Theodore G.

APPLICANT: Dickerson, Harry W.

APPLICANT: Clark, Theodore G.

TITLE OF INVENTION: ICH IMMOBILIZATION ANTIGEN AND FISH

NUMBER OF SEQUENCES: 15

TITLE OF INVENTION: VACCINE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee and Winner

STREET: 5370 Manhattan Circle, Ste. 201

CITY: Boulder

STATE: Colorado

COUNTRY: USA

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Re-lease #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/763,352A

FILING DATE: 19910920

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ferber, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER: 15-91

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303/499-8080

TELEX: 823189

TELEFAX: 303/499-8089

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 414 amino acids

; TYPE: AMINO ACID
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: Protein
 US-07-763-352A-15

Query Match 33.2%; Score 843.5; DB 3; Length 414;
 Best Local Similarity 40.9%; Pred. No. 7.3e-65;
 Matches 196; Conservative 41; Mismatches 131; Indels 111; Gaps 18;
 US-07-763-352A-3

Qy 1 MRNNLVLLISLFLINQIISKNSANCIVPGVGETNTAGQVD---DLSGPANCYNCQKNFYNNAA 56
 Db 1 MKYNLILISLFLINELRAVCPDPGTQ-QGLTDVGADLGT---CVNCRNFYNGG 56

Qy 57 AAFVPGASTCTCPCKQKDAQPNPAPATANLVTCNVKCPAGTAIAGGATDIAITFECV 116
 Db 57 AA-----QEGRANGNPFAAN----- 71

Qy 117 NCRRNFYNNENAPNENAGASTCTACPVBNRYGQGALDTAGNATIVAOQCNVACPTGTAIDDGVT 176
 Db 72 -----WRAARGTVCPOINRVGQSCPTGTAIDDGVT 177

Qy 177 TDYVRSFTECYKCRLNFYNGNN--GNTP----- 71
 Db 118 DVFDRSAAOQCVKCKNFYNGGSPGEAEGVQFAAGAAAAGVAATVISQCVPCQLNK--N 175

Qy 222 VAQATLGNDATTACVNVAQPDGTISAQGVNNVAONTE--CTNCAPFNEYNN----N 272
 Db 176 DSPATAGAQANLATQCSNQCPGTVLDDGVT--LVEFNTSATLCVKCRPNEFYNGGSPQGE 233

Qy 273 APN-----NSTCLCPANKDYGAEATAGGAATLAKCNCNTACPDGTAIAS 320
 Db 234 APGVQVFAAGAAAAGVAAVTSSQCPQCLNKN--DSPATAGAQANLATQCSNQCPGTVLDDGVT 167

Qy 321 GAT-NVYVLOTECLNCAANFYFDGNNFQAGSSRICKACPANKYQAVATAGGTATLIAQCA 379
 Db 293 GVTLFVSNSTIQCSCLKCPVSKTPAH-A-PGNTATQATQCL 350

Qy 380 LECPGATVLTIDGTSTYKQAASECYKCAANFTTKQDWDVAGIDTCTCSNKRLTSGAEA 438
 Db 351 TTCPAGTVLDDGTSTINFEVYASATECTKCSAGFFSKTGTGTAGTDTCTECKKLTSGATA 409

RESULT 4
 US-07-763-352A-3

Sequence 3, Application US-0773352A
 GENERAL INFORMATION:
 APPLICANT: Clark, Theodore G.
 APPLICANT: Dickerson, Harry W.
 TITLE OF INVENTION: ICH IMMOBILIZATION ANTIGEN AND FISH
 TITLE OF INVENTION: VACCINE
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee and Winner
 STREET: 5370 Manhattan Circle, Ste. 201
 CITY: Boulder
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-07/763,352A
 FILING DATE: 19910920
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferber, Donna M.
 REGISTRATION NUMBER: 33,878
 REFERENCE/DOCKET NUMBER: 15-91
 TELECOMMUNICATION INFORMATION:

; TELEPHONE: 303/499-8080
 ; TELEX: 303/499-8089
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 LENGTH: 375 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein

Query Match 29.5%; Score 749; DB 3; Length 375;
 Best Local Similarity 38.4%; Pred. No. 1.2e-56;
 Matches 133; Indels 104; Gaps 15;

Qy 17 QIKSANCIVPGVGETNTAGQVD---DLGPANCYNCQKNFYNNAAFVPGASTCTCPQPK 72
 Db 1 EFRAYVCPDPQTQ-AGLTDVGADLGT--CVNCRNFYNGGAA----- 42

Qy 73 RDAGAQNPAPATANLVTCNVKCPAGTAIAGGATDIAITCVRNCRNFYNNENAPNENA 132
 Db 43 -OGEANGNQFAAN----- 57
 ; -NA

Qy 133 GASTCTACPVNRVYGGALTAGNAATIVACQNVAQCPGTGALDGGVTTDYVRSSTECYKCRLN 192
 Db 58 ARGICVPCQINRVGSVTAGDLATLATOCSCTOPTGALDGGVTFEDRSAAQCYKCKPN 117

Qy 193 EYYNGNNNGNTPFNNGKSQCTPCPAIKPANVQAATLGNDATTAQCNVACPPGTISAGVN 252
 Db 118 FYYNG----- 167

Qy 253 NWVQANTE--CTNCAPFNEYNN----NAPN--ENPG----- 291
 Db 168 -EVENTSATLCVKCRPNEYNGSPGEAEPGVQVAAAGVAAVTSCCPVPCQLNKN 225

Qy 292 YGABTAGGAAATLAKQCNNTACPDGTAIASGAT-NVYVLOTECLNCAANFYFDGNNFQAGS 350
 Db 226 -DSPATAGAQANLATQCSSTQCPGTATQDGTVLVSNSSTQSQCTANYFNG-DEAGK 283

Qy 351 SRCACPANKVQGAVATAGGTATLIAQCALGPAGTVLDTSTYKQAASECYKCAANF 410
 Db 284 SQCLKCPVSKTPAH-A-PGNTATQATQCLTGPAGTVLDDGTSTNEVASATECTKCSAGE 342

RESULT 5
 PCT-US01-06960-2

; Sequence 2, Application PC/TU0106960
 ; GENERAL INFORMATION:
 ; APPLICANT: The Trustees of Columbia University in the City of New York,
 ; APPLICANT: et al.
 ; TITLE OF INVENTION: Melanoma Differential Associated Gene-5 (mda-5), Promoter
 ; TITLE OF INVENTION: and Uses Thereof
 ; FILE REFERENCE: 0575/60849-A-PCT
 ; CURRENT APPLICATION NUMBER: PCT/US01/06960
 ; NUMBER OF SEQ ID NOS: 3
 ; SEQ ID NO: 2
 ; LENGTH: 3131
 ; TYPE: PRT
 ; ORGANISM: Human
 ; SOFTWARE: Patentin version 3.0

Query Match 9.9%; Score 251; DB 1; Length 311;
 Best Local Similarity 24.7%; Pred. No. 6.6e-12;
 Matches 119; Conservative 6; Mismatches 177; Indels 180; Gaps 19;

Qy 23 CPVGETNTAGQVDDLGPANCVN- 46
Db 381 CAGCTTCATAGTAGAGCTCTGGATAAGTGCATGGAGGAACTGTGACATTGA 440
Qy 47 ---CQKNEYNNAAAFVGAST---CTPCPKDKDAGAQNPATANLVTCNVKCPAGT 99
Db 441 AGACA-----GAAACCGGATGCTGTC-----AGAAAACAAATGAAATGAGGT 489
Qy 100 AIAAGATDYAAITECVNCRINFYNNENAPFNFGASCTACPVRNGALTAGNATIVA 159
Db 490 GTAAGA-----GAGCTACTAAAAA-AGGATGTGCGAGAA 522
Qy 160 QCNVACPTGTALDDGVTDYVRSFTECYKRLNFYVNGNNTPFPNGKSQCTPCPAIKP 219
Db 523 GAAAPCTGGT-----CTCGCAATTCTGATGTT-----CTTC----- 556
Qy 220 ANVAGTLGNDATITACQCNVACPDTISAAQGVNNWVAQNTCT-----NCAPNFYNN 271
Db 557 -GTCACAAAGAACATGAACTGCTGTC-----AGAAAACAAATGAAATGAGGT 489
Qy 272 NAPNPNGNSTCLCPANKDGYAESTAG-GAATLAQCNIAACPDTGTAIASGATNYVILQT 330
Db 610 -----GAAAGCAATGGAGAGATTGAGAAATTATC-ACAAGTGTGTT----- 651
Qy 331 ECLNCANANFYFDGNNFQAGSSRCKACPANKV-----OGAVATA 368
Db 652 -CCTCAAG-----TGGAGAGCAACTCTTCAACCACAGCTTCAGGAAAGGA 707
Qy 369 GCTATLJAQCALECPAGTVLTDGTISTYKQASEVCVK--AANFTTQDWTWAGIDCT 426
Db 708 GTCCTGGGCA-----TGAGAGA-----TAACTCATCAGAAATCATCTTTCAGATTCT 756
Qy 427 SC 428 :
Db 757 TC 758 :

RESULT 7
US-09-515-363B-2 ; Sequence 2, Application US/09515363B
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul
; TITLE OF INVENTION: Melanoma Differential Associated Gene-5 (mda-5), Promoter and
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 0575/60849
; CURRENT APPLICATION NUMBER: US/09/515,363B
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 3131
; TYPE: PRT
; ORGANISM: Human
US-09-515-363B-2

RESULT 6
US-09-515-363-2 ; Sequence 2, Application US/09515363
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul
; TITLE OF INVENTION: Melanoma Differential Associated Gene-5 (mda-5), Promoter and use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 0575/60849
; CURRENT APPLICATION NUMBER: US/09/515,363
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 3131
; TYPE: PRT
; ORGANISM: Human
US-09-515-363-2

Query Match 9.9%; Score 251; DB 19; Length 3131;
Best Local Similarity 24.7%; Pred. No. 6.e-12; Mismatches 177; Indels 180; Gaps 19;

Qy 23 CPVGETNTAGQVDDLGPANCVN----- 46
Db 381 CAAGCTCTAGTAGAGACGCTTGGATAAGTGCATGGAGGAACTGTGACATTGA 440
Qy 47 ---CQKNEYNNAAAFVGAST---CTPCPKDKDAGAQNPATANLVTCNVKCPAGT 99
Db 441 AGACA-----GAAACCGGATGCTGTC-----AGAAAACAAATGAAATGAGGT 489
Qy 100 AIAAGATDYAAITECVNCRINFYNNENAPFNFGASCTACPVRNGALTAGNATIVA 159
Db 490 GTAAGA-----GAGCTACTAAAAA-AGGATGTGCGAGAA 522
Qy 160 QCNVACPTGTALDDGVTDYVRSFTECYKRLNFYVNGNNTPFPNGKSQCTPCPAIKP 219

Query Match 9.9%; Score 251; DB 19; Length 3131;
Best Local Similarity 24.7%; Pred. No. 6.e-12; Mismatches 177; Indels 180; Gaps 19;

Qy 220 ANVAGTLGNDATITACQCNVACPDTISAAQGVNNWVAQNTCT-----NCAPNFYNN 271
Db 557 -GTCACAAAGAACATGAACTGCTGTC-----AGAAAACAAATGAAATGAGGT 489
Qy 272 NAPNPNGNSTCLCPANKDGYAESTAG-GAATLAQCNIAACPDTGTAIASGATNYVILQT 330
Db 610 -----GAAAGCAATGGAGAGATTGAGAAATTATC-ACAAGTGTGTT----- 651
Qy 331 ECLNCANANFYFDGNNFQAGSSRCKACPANKV-----OGAVATA 368
Db 652 -CCTCAAG-----TGGAGAGCAACTCTTCAACCACAGCTTCAGGAAAGGA 707
Qy 369 GCTATLJAQCALECPAGTVLTDGTISTYKQASEVCVK--AANFTTQDWTWAGIDCT 426
Db 708 GTCCTGGGCA-----TGAGAGA-----TAACTCATCAGAAATCATCTTTCAGATTCT 756
Qy 427 SC 428 :
Db 757 TC 758 :

Query Match 9.9%; Score 251; DB 19; Length 3131;
Best Local Similarity 24.7%; Pred. No. 6.e-12; Mismatches 177; Indels 180; Gaps 19;

Qy 23 CPVGETNTAGQVDDLGPANCVN----- 46
Db 381 CAAGCTCTAGTAGAGACGCTTGGATAAGTGCATGGAGGAACTGTGACATTGA 440
Qy 47 ---CQKNEYNNAAAFVGAST---CTPCPKDKDAGAQNPATANLVTCNVKCPAGT 99
Db 441 AGACA-----GAAACCGGATGCTGTC-----AGAAAACAAATGAAATGAGGT 489
Qy 100 AIAAGATDYAAITECVNCRINFYNNENAPFNFGASCTACPVRNGALTAGNATIVA 159
Db 490 GTAAGA-----GAGCTACTAAAAA-AGGATGTGCGAGAA 522
Qy 160 QCNVACPTGTALDDGVTDYVRSFTECYKRLNFYVNGNNTPFPNGKSQCTPCPAIKP 219

Query Match 9.9%; Score 251; DB 19; Length 3131;
Best Local Similarity 24.7%; Pred. No. 6.e-12; Mismatches 177; Indels 180; Gaps 19;

Qy 220 ANVAGTLGNDATITACQCNVACPDTISAAQGVNNWVAQNTCT-----NCAPNFYNN 271
Db 557 -GTCACAAAGAACATGAACTGCTGTC-----AGAAAACAAATGAAATGAGGT 489
Qy 272 NAPNPNGNSTCLCPANKDGYAESTAG-GAATLAQCNIAACPDTGTAIASGATNYVILQT 330
Db 610 -----GAAAGCAATGGAGAGATTGAGAAATTATC-ACAAGTGTGTT----- 651
Qy 331 ECLNCANANFYFDGNNFQAGSSRCKACPANKV-----OGAVATA 368
Db 652 -CCTCAAG-----TGGAGAGCAACTCTTCAACCACAGCTTCAGGAAAGGA 707
Qy 369 GCTATLJAQCALECPAGTVLTDGTISTYKQASEVCVK--AANFTTQDWTWAGIDCT 426
Db 708 GTCCTGGGCA-----TGAGAGA-----TAACTCATCAGAAATCATCTTTCAGATTCT 756
Qy 427 SC 428 :
Db 757 TC 758 :

Query Match 9.9%; Score 251; DB 19; Length 3131;
Best Local Similarity 24.7%; Pred. No. 6.e-12; Mismatches 177; Indels 180; Gaps 19;

Qy 23 CPVGETNTAGQVDDLGPANCVN----- 46
Db 381 CAAGCTCTAGTAGAGACGCTTGGATAAGTGCATGGAGGAACTGTGACATTGA 440
Qy 47 ---CQKNEYNNAAAFVGAST---CTPCPKDKDAGAQNPATANLVTCNVKCPAGT 99
Db 441 AGACA-----GAAACCGGATGCTGTC-----AGAAAACAAATGAAATGAGGT 489
Qy 100 AIAAGATDYAAITECVNCRINFYNNENAPFNFGASCTACPVRNGALTAGNATIVA 159
Db 490 GTAAGA-----GAGCTACTAAAAA-AGGATGTGCGAGAA 522
Qy 160 QCNVACPTGTALDDGVTDYVRSFTECYKRLNFYVNGNNTPFPNGKSQCTPCPAIKP 219

Query Match 9.9%; Score 251; DB 19; Length 3131;
Best Local Similarity 24.7%; Pred. No. 6.e-12; Mismatches 177; Indels 180; Gaps 19;

Qy 220 ANVAGTLGNDATITACQCNVACPDTISAAQGVNNWVAQNTCT-----NCAPNFYNN 271
Db 557 -GTCACAAAGAACATGAACTGCTGTC-----AGAAAACAAATGAAATGAGGT 489
Qy 272 NAPNPNGNSTCLCPANKDGYAESTAG-GAATLAQCNIAACPDTGTAIASGATNYVILQT 330
Db 610 -----GAAAGCAATGGAGAGATTGAGAAATTATC-ACAAGTGTGTT----- 651
Qy 331 ECLNCANANFYFDGNNFQAGSSRCKACPANKV-----OGAVATA 368
Db 652 -CCTCAAG-----TGGAGAGCAACTCTTCAACCACAGCTTCAGGAAAGGA 707
Qy 369 GCTATLJAQCALECPAGTVLTDGTISTYKQASEVCVK--AANFTTQDWTWAGIDCT 426
Db 708 GTCCTGGGCA-----TGAGAGA-----TAACTCATCAGAAATCATCTTTCAGATTCT 756
Qy 427 SC 428 :
Db 757 TC 758 :

Query Match 9.9%; Score 251; DB 19; Length 3131;
Best Local Similarity 24.7%; Pred. No. 6.e-12; Mismatches 177; Indels 180; Gaps 19;

Qy 23 CPVGETNTAGQVDDLGPANCVN----- 46
Db 381 CAAGCTCTAGTAGAGACGCTTGGATAAGTGCATGGAGGAACTGTGACATTGA 440
Qy 47 ---CQKNEYNNAAAFVGAST---CTPCPKDKDAGAQNPATANLVTCNVKCPAGT 99
Db 441 AGACA-----GAAACCGGATGCTGTC-----AGAAAACAAATGAAATGAGGT 489
Qy 100 AIAAGATDYAAITECVNCRINFYNNENAPFNFGASCTACPVRNGALTAGNATIVA 159
Db 490 GTAAGA-----GAGCTACTAAAAA-AGGATGTGCGAGAA 522
Qy 160 QCNVACPTGTALDDGVTDYVRSFTECYKRLNFYVNGNNTPFPNGKSQCTPCPAIKP 219

Db 652 -CCTCAAG---TGGAGGAGCAACTCTTCAACCCACAGTCAGGCCAAATCTGGAGAAGGA 707
 Qy 369 GGTATLIAQCALECPAGTVLTDGTTSTYKQAAASEFVKC--AANFYTTKOTDWYAGIDCT 426
 Db 708 GGTCTGGGCA-----TGAGAA--TAACTCATAGAAATCATCTTGGAGATCT 756
 Qy 427 SC 428
 Db 757 TC 758

RESULT 8
 ; Sequence 1, Application US/08028021
 ; GENERAL INFORMATION:
 ; APPLICANT: THOMPSON, JOHN F.
 ; TITLE OF INVENTION: PROMOTOR AND GENE FOR HUMAN
 ; TITLE OF INVENTION: CHOLESTEROL
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PETER C. RICHARDSON
 ; STREET: 235 EAST 42ND STREET, 42ND STREET
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10017-5755
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/028,021
 ; FILING DATE: 08-MAR-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STRASSBURGER, PHILIP C.
 ; REGISTRATION NUMBER: 34,258
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 573-5311
 ; TELEX: (212) 573-1939
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3880 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-028-021-1

Query Match 9.7% Score 245.5; DB 4; Length 3880;
 Best Local Similarity 25.8%; Pred. No. 2.6e-11; Mismatches 9; Indels 123; Gaps 21;
 Matches 115; Conservative

Db 21 ANCAGTETNTAGVDDIGTPANCVNQKNEYNNAAAAYFGASTC-----TPCP 70
 Db 2849 ATCATATCTAA-----GTTGTCCTC-----ATGCCCATAGCTTCT 2847

Qy 71 QKDAGAQNPATANLYTQC-NVKCPAGTATAAGGATDYAAITECVNCRINFYNENAPN 129
 Db 2888 ATCCATGTTTTTCAATACATGTTTCTCCAT-----TGGA 2943
 Qy 130 FNAGASTCTACPYNRVGGALTAGN-ATIVAQCNVACPTGTAIDGVTIDYVRSETECYK 188
 Db 2944 ATGAAATCTCCAT-----TAGATTAGAAATCTGCATCTT-----TAATG 2987

Qy 189 CRNFYYNGNGNTPNPGKSCUTCPCPAIK-PANVAQATLGNDATITACQNVACPDGTI 246
 Db 2988 CTGCAACTGGAAATCTGCATCTTGAAGATCTTGGCACGTA 3026

Qy 247 SAAGVNNWVAQNTECTNCAPNFYNNNAPNINPGNSTCLPCPANKDYGAEATAGGAATLAK 306
 Db 3027 ATAAA-----TACT-CAT-CTAAATATTGTTGTCACA-----GAATTAAGATTTGG 3072
 Qy 307 QCNIAPDGTAIASGATNTYILQPECLNANFYFDGNNEQGSSRCKACPANKVQGAVA 366
 Db 3073 AAGAACAGAGGCCAAT-----TGTTACTAG-----TGTTACTCTG---AGTA 3114
 Qy 367 TAGGTATLIAQCALECPAG-----TVLTDTGTTSTYKQAASECYKCAANFYTKQTD 417
 Db 3115 AAGGAGT--PGCATGGTAGGAAATTATATAGATGTTCACTTCCACCAAGATATGTT 3172
 Qy 418 WVAG--IDCTC--SCNKKUTSGAF 438
 Db 3173 TTAGTTAGCTTAACCTACTTGAAA 3197

RESULT 9
 US-09-791-932-40
 ; Sequence 40, Application US/0971932
 ; GENERAL INFORMATION:
 ; APPLICANT: Vogeli, Gabriel
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Hiebsch, Ronald R.
 ; APPLICANT: Lind, Peter
 ; APPLICANT: Kaytes, Paul S.
 ; APPLICANT: Ruff, Valerie
 ; APPLICANT: Huff, Rita M.
 ; APPLICANT: Wood, Linda S.
 ; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related
 ; FILE REFERENCE: 00325 US1
 ; CURRENT APPLICATION NUMBER: US/09/791 932
 ; CURRENT FILING DATE: 2001-02-23
 ; PRIORITY NUMBER: 60/184,305
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIORITY NUMBER: 60/184,304
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIORITY NUMBER: 60/184,303
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIORITY NUMBER: 60/184,397
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIORITY NUMBER: 60/184,247
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIORITY NUMBER: 60/184,880
 ; PRIOR FILING DATE: 2000-03-13
 ; PRIORITY NUMBER: 60/217,369
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIORITY NUMBER: 60/217,370
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIORITY NUMBER: 60/218,492
 ; PRIOR FILING DATE: 2000-07-20
 ; PRIORITY NUMBER: 60/186,810
 ; PRIOR FILING DATE: 2000-03-03
 ; PRIORITY NUMBER: 60/188,064
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIORITY NUMBER: 60/213,861
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIORITY NUMBER: 60/194,344
 ; PRIOR FILING DATE: 2000-04-03
 ; PRIORITY NUMBER: 60/218,337
 ; PRIORITY NUMBER: 60/218,337
 ; NUMBER OF SEQ ID NOS: 184
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 40
 ; LENGTH: 544
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-791-932-40

Query Match 9.5%; Score 242.5; -DB 21; Length 544;
 Best Local Similarity 24.5%; Pred. No. 4e-12;
 Matches 11; Conservative 11; Mismatches 183; Indels 173; Gaps 22;

SEQUENCE CHARACTERISTICS:
 LENGTH: 2826 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 PCT-US97-17746-50

Query Match 9.4%; Score 238.5; -DB 1; Length 2826;
 Best Local Similarity 26.6%; Pred. No. 7.2e-11;
 Matches 119; Conservative 229; Indels 93; Gaps 22;

Query 20 SPNCP---VGTEETNTAGQVDDLGTPANCY--NCQKNFYYNNAAAFVPGASTCPCPORKK 73
 Db 273 ATCTGTGGTGAATGTCAGATTGAAAGCAAGTCACCCAGAGCTC--- 328

Query 74 DGAQQPNNPATAANLYTQCNVKCPAGTAIAGATDY-AAGITECYNCRINFYENAPNPN 131
 Db 329 ---AACZTCAGAC---CAGTCAGGGTGTGGAAACTACTTCACATGACTTGAT 377

Query 132 AGCTCTCA-CIVNRYG---GALTAGNAA-----TVAQCNVACPTGTLDDGVFTD 178
 Db 378 GGCGCCTATGCAGGTGAAAGCTTGAGAAAGGTATGCCATGTGTTGTTGIGGAT- 435

Query 179 YVRSFTECVKCRKINFYNGNNNTIPNPKSQCTCPAIKPANVAQATLGNDNATAQCN 238
 Db 436 -GATTTCTCC-----AGATTACCTGGTCACAATT- -TATCAGAGAAATAGACA 484

Query 239 VACPDP---TISAAAGVNNWVAQNT----ECTNC-APNYYNNAPNPNFGNSCLCPCP 287
 Db 485 CCTTTGAAGTATCAGGAGTGAAGCTTAAGACTCAAAGCTCAAGCTCAAGTCATCA 544

Query 288 ANFDYGAATAGATGAAATLARQHNIACPGTAIASGAGNYVILQTECLNAAANFYFDGNNFQ 347
 Db 545 AGA-GAATCAGGAGTGA---CCATGGCAGAGGTTGAAACAGCAAG---TTTACT 594

Query 348 AGSSRCXACPANKVQGAVATAGSTATIAQCLECPATVLLDGTSYSTKAAASECVKA 407
 Db 595 GAATTCGACATCTGA---AGSCAT---CCTCTCATGA ---GTCT ---CTGCA 636

Query 408 ANFYTTKQTDWWAGIDTCSNKL 435
 Db 637 GCCATT---ACACCAAAATGG 659

RESULT 11
 PCT-US97-17746-50
 ; Sequence 50, Application PC/TUS9717746

; GENERAL INFORMATION:
 ; APPLICANT: Laten, Howard M.
 ; TITLE OF INVENTION: PLANT RETROVIRAL POLYNUCLEOTIDES AND
 ; METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray and Borun
 ; STREET: 233 South Wacker Drive/6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/17746
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; REFILEDOCKET NUMBER: 27013/33214 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; INFORMATION FOR SEQ ID NO: 50:

RESULT 11
 US-09-254-776-50
 ; Sequence 50, Application US/09254776
 ; GENERAL INFORMATION:
 ; APPLICANT: Laten, Howard M.
 ; TITLE OF INVENTION: PLANT RETROVIRAL POLYNUCLEOTIDES AND
 ; METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray and Borun
 ; STREET: 233 South Wacker Drive/6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/254,776
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; REFILEDOCKET NUMBER: US/09/254,776
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; INFORMATION FOR SEQ ID NO: 50:

REFERENCE/DOCKET NUMBER: 27013/33214 US
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 SEQUENCE FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2826 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-09-254-776-50

Query Match Score 9.4%; Best Local Similarity 25.7%; Pred. No. 2.1e-11; Mismatches 9; Indels 139; Gaps 19;

Qy 20 SANCP---VGETTNTAGQVDDLGTPANCY-INCOKNFYNNAAAFVGCASTCPCPKK 73
 Db 273 ATCTGTGTAATGTCAGATTGAAAGCAAGTCAAGATGTCACACCAGAAGTTTC--- 328

Qy 74 DAGAQPNPPTANLYTQCNVKCPGATAAGGATDY-AAIITEVNCNINFYNEAPNEN 131
 Db 329 -----AACATCACAG---CACTTCCAGGGTCTGGAAACTACTTCACATGGACTGAT 377

Qy 132 AGASTCTA--CPVNRVG--GALTGNAA-----TIVACQNVNACPTGTAIDDGYTID 178
 Db 378 GGCCCTATGCAAGTGAAGCTGGTGAAGAAAAGGATGCCATGTTGTTGGAT-- 435

Qy 179 YRSPFTECVKRLNFYYNGNNTPFNPKGKSQCTCPAIPKPAVQAQLGNDAITPAQCN 238
 Db 436 --GATTCTCC----AGATTAACCTGGTCAACTCT--TATCAGAGAAATCAGACA 484

Qy 239 VACPDTG----TISAGVNNWQANT----ECTNC-APNFYNNAPNPNPONSTCLPCP 287
 Db 485 CCTTGAAAGTATCAAGGAGTTGAGCTTAAGACTCAAAGAGAAAAGACTGTCATCA 54.4

Qy 288 ANKDGAETAGGAATLARQCNICPDGTIAASGATNVILQECLCAANFYDGNNFQ 347
 Db 545 AGA-GAATAGGACTGA---CCATCGCAGAGTGTGAAAACAGCAAG--TTTACT 594

Qy 348 AGSSRKACPANKYQGAVATGGTATLIAQCALECPAGTVLTDGTTSYKAASECVKCA 407
 Db 595 GAATTCCTGCACATCTGA---AGGCAT---CCTCATGA---GTTCT---TGCA 636

Qy 408 ANFTTKQIDWVAGIDTCNSNKKLTSG 435
 Db 637 GCATC----ACACACACACAAATGG 659

RESULT 1.3
 US-09-436-063-5
 Sequence 5, Application US/09436063A
 GENERAL INFORMATION:
 ; APPLICANT: Bamber, Bruce A.
 ; INVENTION: Nematoide Neuromuscular Junction GABA Receptors and Methods Related Thereto
 ; TITLE OF INVENTION: Nematoide Neuromuscular Junction GABA Receptors and Methods Related Thereto
 ; CURRENT APPLICATION NUMBER: US/09/436, 063A
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 1917
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-09-436-063-5

Query Match Score 9.2%; Best Local Similarity 25.4%; Pred. No. 1.3e-10; Mismatches 115; Indels 90; Gaps 18;

Qy 23 CPVGTEINTAGQVDDLGTPANCYOKNFYNNAAAFVPGASTC---STCTCPQ 71
 Db 622 CTCACTTACCGTCGGACTAGCTACCTGGATAAGACTGTGAAACCCGACACTTC 681

Qy 72 KKDAQGPNPATANLYTQCNVKCPGATAAGGATDYAALITECVNCRINFYNEAPNEN 131
 Db 682 AAATGAAA-AAGAAATCATCTTCCACTT---GGCAACACACATAAC---T 725

Qy 132 AGASTCTACPYNRGGTATCAGTCAAGGAAAGTAAAGTAAAGTACAGTCA 783
 Db 726 CGTTCCCTCGPATCGAG-GTTGATGGAAAGGGTTATACTAGCAAAGTAAAGTAC 783

Query Match 9.4%; Score 237.5; DB 1; Length 914;
 PCT-US00-08561-47
 ; GENERAL INFORMATION:
 ; APPLICANT: HSU, Daniel, K.
 ; APPLICANT: LIU, Fu-Tong
 ; APPLICANT: DOWLING, Christopher, A.
 ; TITLE OF INVENTION: GALECTIN EXPRESSION IS INDUCED IN CIRRHOTIC LIVER AND HEPATOCELLULAR CARCINOMA
 ; FILE REFERENCE: DANFSU 001VPC
 ; CURRENT APPLICATION NUMBER: PCT/US00/08561
 ; CURRENT FILING DATE: 2000-03-29
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 47
 ; LENGTH: 914
 ; TYPE: PRT
 ; ORGANISM: human
 PCT-US00-08561-47

RESULT 14
 US-0-436-063C-5
 ; Sequence 5, Application US/09436063C
 ; GENERAL INFORMATION:
 ; APPLICANT: Bamber, Bruce
 ; ATTORNEY: Jorgensen, Erik
 ; TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and Methods Related Thereto
 ; FILE REFERENCE: P-1095corrected
 ; CURRENT APPLICATION NUMBER: US/09/436, 063C
 ; CURRENT FILING DATE: 1999-11-08
 ; PRIOR APPLICATION NUMBER: 60/107727
 ; PRIOR FILING DATE: 1998-11-09
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 5
 ; LENGTH: 1917
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 ; US-09-627-650-5

Query Match 9.2%; Score 233; DB 18; Length 1917;
 Best Local Similarity 25.4%; Pred. No. 1.e-10;
 Matches 115; Conservative 10; Mismatches 238; Indels 90; Gaps 18;

QY 23 CPVCTETNTAGQVDLGLTPANCYNCQRNEYNNAAAFVPGA-----STCPCPQ 71
 Db 622 CTCACCTAACGGCCGAGTAGACTTCTGGATAGCTGTGGAAACCGACAGCTTCITCCC 681
 QY 72 KKDAGAQPNPATTANLVTOCNVKCPAGTAIAGGATDYAAIITECVNCRINFYNNAPNFN 131
 Db 682 AAATGAAA -AGAAATCATCTCCACTT ---GGCAACACACATAAC-----T 725
 QY 132 AGASTCTACPVNRGGALTAGNAATIVQCN ---VACPTGALDDGVTTDVRSETEC 186
 Db 726 CGTTCCTCTCATCAG ---GGTGTGGAGCTAGCTGGATAGCTGGAAACCGACAGCTTCITCCC 681
 QY 187 WKCRLNFYNYNGNNTPENPGKSOCTPCPAIKPANVAQATLGNDATIT-AQC---NVA 240
 Db 784 TGCAA ---CGTGTCCAATGACCTGAAGCTGAAGCTAACACTGCAA 783
 QY 241 CPDGTISAAGVNWNNAQNTCTNAPFVNNAFPNFGNSCLPCPANKDYGAERTAGG 300
 Db 839 CTGGAATTCAGCTACGGCTACA-----GTATCCTCGA----CATATTAG 880
 QY 301 AATLAQCNIACPDGTAISG ---ATNVYVLOTCLNCAANFYFDGNNFQAGSSRCKACP 357
 Db 881 TAGCTCCAAATGGACGAAAGACTCTCAAATGTAA 838
 QY 241 CPDGTISAAGVNWNNAQNTCTNAPFVNNAFPNFGNSCLPCPANKDYGAERTAGG 300
 Db 839 CTGGAATTCAGCTACGGCTACA-----GTATCCTCGA----CATATTAG 880
 QY 187 WKCRLNFYNYNGNNTPENPGKSOCTPCPAIKPANVAQATLGNDATIT-AQC---NVA 240
 Db 784 TGCAA -AGAAATCATCTCCACTT ---CGTGTGGAGCTAGCTGGAAACCGACAGCTTCITCCC 681
 QY 726 CGTTCCTCTCATCAG ---GGTGTGGAGCTAGCTGGATAGCTGTGGAAACCGACAGCTTCITCCC 681
 QY 187 WKCRLNFYNYNGNNTPENPGKSOCTPCPAIKPANVAQATLGNDATIT-AQC---NVA 240
 Db 784 TGCAA -AGAAATCATCTCCACTT ---CGTGTGGAGCTAGCTGGAAACCGACAGCTTCITCCC 681
 QY 241 CPDGTISAAGVNWNNAQNTCTNAPFVNNAFPNFGNSCLPCPANKDYGAERTAGG 300
 Db 839 CTGGAATTCAGCTACGGCTACA-----GTATCCTCGA----CATATTAG 880
 QY 301 AATLAQCNIACPDGTAISG ---ATNVYVLOTCLNCAANFYFDGNNFQAGSSRCKACP 357
 Db 881 TAGCTCCAAATGGACGAAAGACTCTCAAATGTAA 838
 QY 358 ANKVQGAVAT -----AGGT -ATLIAQCALEC -- -PAGTVLTDGTTSVYKQAASEC 403
 Db 934 GTTGTACTTCAAGGCTCATCATACGCCAAAGCTTACTGTCAGGAGATA 993
 QY 404 VKCAANFYTTKOTDWVAGIDFCSCNKKLTSGA 436
 Db 994 TTCCCGCCT -- -TTGCTGGTCTCCCTTCAA 1023

Search completed: December 26, 2001, 10:38:06
 Job time: 187 sec